STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 15/33, 128C
Source: 1FWO, Date Processed by STIC: 1//22/2004

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 4.4.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
 U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
 Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 10/535, /28C			
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE				
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."			
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.			
3Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.			
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.			
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.			
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.			
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.			
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number			
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.			
0Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)			
Use of <220>	Sequence(s)missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules			
PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.			
3 Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid			



IFWO

RAW SEQUENCE LISTING DATE: 11/22/2006 PATENT APPLICATION: US/10/535,128C TIME: 11:26:26

Input Set : A:\BU-0094.ST25.txt

Output Set: N:\CRF4\11222006\J535128C.raw

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3 <110> APPLICANT: Collins, et. al
 5 <120> TITLE OF INVENTION: CIS/Trans Riboregulators
 7 <130> FILE REFERENCE: 0079571-0094
 9 <140> CURRENT APPLICATION NUMBER: 10/535,128C
10 <141> CURRENT FILING DATE: 2005-05-16
12 <160> NUMBER OF SEQ ID NOS: 59
                                                        Does Not Comply
14 <170> SOFTWARE: PatentIn version 3.2
                                                        Corrected Diskette Needed
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 11
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial
21 <220> FEATURE:
22 <223> OTHER INFORMATION: Consensus sequence
24 <400> SEQUENCE: 1
                                                                              11
25 gccgaccaug c
28 <210> SEQ ID NO: 2
                                                            what is Haterial?

What is Material?

Of genetic Material?

Use your Summary

Sheet).
29 <211> LENGTH: 18
30 <212> TYPE: DNA
31 <213> ORGANISM: Artificial
33 <220> FEATURE:
34 <223> OTHER INFORMATION: (Nuclear Acid sequence
36 <400> SEQUENCE: 2
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41 <211> LENGTH: 19
42 <212> TYPE: DNA
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46 <223> OTHER INFORMATION: Cis-Repressive
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52 <210> SEQ ID NO: 4
53 <211> LENGTH: 20
54 <212> TYPE: DNA
55 <213> ORGANISM: Artificial
57 <220> FEATURE:
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67 <213> ORGANISM: Artificial

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/535,128C

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Input Set : A:\BU-0094.ST25.txt

Output Set: N:\CRF4\11222006\J535128C.raw

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Input Set : A:\BU-0094.ST25.txt

Output Set: N:\CRF4\11222006\J535128C.raw

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Input Set : A:\BU-0094.ST25.txt

Output Set: N:\CRF4\11222006\J535128C.raw

216 <400> SEQUENCE: 17 217 ctaccattca cctcttggat ttgggtatta aagaggagaa aggtaccatg 50 220 <210> SEQ ID NO: 18 221 <211> LENGTH: 50 222 <212> TYPE: DNA 223 <213> ORGANISM: Artificial 225 <220> FEATURE: 226 <223> OTHER INFORMATION: Cis-Repressive RNA Constructs 228 <400> SEQUENCE: 18 50 229 ctaccattca cctcttggat ttgggtatta aagaggagaa aggtaccatg 232 <210> SEQ ID NO: 19 7 Same Error 233 <211> LENGTH: 70 234 <212> TYPE: DNA 235 <213> ORGANISM: Artificial 237 <220> FEATURE: 238 <223> OTHER INFORMATION:/Construct Sequence 240 <400> SEQUENCE: 19 241 acacccaaat taaagaggag aaaggtagtg gtggttaatg aaaattaact tactactacc 243 ttttcttaga 70 246 <210> SEQ ID NO: 20 247 <211> LENGTH: 62 248 <212> TYPE: DNA 249 <213> ORGANISM: Artificial 251 <220> FEATURE: 252 <223> OTHER INFORMATION Construct Sequence 254 <400> SEQUENCE: 20 255 acgccccaat aaggaggata gagtggtggt taatgaaaat taacttacta cttagtttta 60 257 ga 62 260 <210> SEQ ID NO: 21 261 <211> LENGTH: 69 262 <212> TYPE: DNA 263 <213> ORGANISM: Artificial 265 <220> FEATURE: 266 <223> OTHER INFORMATION: Construct Sequence 268 <400> SEQUENCE: 21 269 acacccaaat cctagggaga atggtagtgg tggttaatga aaattaactt actactactt 60 271 tttcataga 274 <210> SEQ ID NO: 22 275 <211> LENGTH: 67 276 <212> TYPE: DNA 277 <213> ORGANISM: Artificial 279 <220> FEATURE: 280 <223> OTHER INFORMATION; Construct Sequence 282 <400> SEQUENCE: 22 283 acacccaaat tatgagcaga ttggtagtgg tggttaatga aaattaactt actactactt 60 67 285 tcttaga 288 <210> SEQ ID NO: 23 289 <211> LENGTH: 71 290 <212> TYPE: DNA

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313	atatctctag a		71
316	<210> SEQ ID NO: 25		
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319	<213> ORGANISM: Artificial		
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322	<223> OTHER INFORMATION Construct Sequence		
324	<400> SEQUENCE: 25		
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330	<210> SEQ ID NO: 26		
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336	<223> OTHER INFORMATION: (Construct Sequence		
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Output Set: N:\CRF4\11222006\J535128C.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27 Seq#:28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51 Seq#:52,53,54,55,56,57,58,59 VERIFICATION SUMMARY

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